

(D) analyzing expression patterns of genes derived from a coryneform bacterium, or

(E) identifying a gene homologous to a gene derived from a coryneform bacterium,

said method comprising:

(a) producing a polynucleotide array by adhering to a solid support at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions, and third polynucleotides comprising a sequence of 10 to 200 continuous bases of the first or second polynucleotides,

(b) incubating the polynucleotide array with at least one of a labeled polynucleotide derived from a coryneform bacterium, a labeled polynucleotide derived from a mutant of the coryneform bacterium or a labeled polynucleotide to be examined, under hybridization conditions,

(c) detecting any hybridization, and

(d) analyzing the result of the hybridization;

said coryneform bacterium being optionally a microorganism belonging to the genus *Corynebacterium*, optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, or *Corynebacterium ammoniagenes*; the genus *Brevibacterium*, or the genus *Microbacterium*;

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wherein said polynucleotide derived from a coryneform bacterium, polynucleotide derived from a mutant of the coryneform bacterium or polynucleotide to be examined is optionally a gene relating to the biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof; and

said polynucleotide to be examined is optionally derived from *Escherichia coli*.

70. (new) A polynucleotide array, comprising:

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at least two polynucleotides selected from the group consisting of first polynucleotides comprising the nucleotide sequence represented by any one of SEQ ID NOS:1 to 3501, second polynucleotides which hybridize with the first polynucleotides under stringent conditions, and third polynucleotides comprising 10 to 200 continuous bases of the first or second polynucleotides, and
a solid support adhered thereto.

71. (new) A nucleic acid sequence comprising

a polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1 or a polynucleotide having a homology of at least 80% with the polynucleotide; a polynucleotide comprising any one of the nucleotide sequences represented by SEQ ID NOS:2 to 3431, or a polynucleotide which hybridizes with the polynucleotide under stringent conditions;

a polynucleotide encoding a polypeptide having any one of the amino acid sequences represented by SEQ ID NOS:3502 to 6931, or a polynucleotide which hybridizes therewith under stringent conditions; a polynucleotide which is present in the 5' upstream or 3' downstream of a polynucleotide comprising the nucleotide sequence

of any one of SEQ ID NOS:2 to 3431 in a whole polynucleotide comprising the nucleotide sequence represented by SEQ ID NO:1, and has an activity of regulating an expression of the polynucleotide;

a polynucleotide comprising 10 to 200 continuous bases in the nucleotide sequence of the polynucleotide of any one of claims 7 to 10, or a polynucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising 10 to 200 continuous based; or

a recombinant DNA comprising at least one of any said polynucleotides.

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cont 72. (new) A transformant comprising a nucleic acid sequence of claim 71.

73. (new) A method for producing a polypeptide, comprising:

culturing the transformant of claim 72 in a medium to produce and accumulate a polypeptide encoded by said polynucleotide in the medium, and recovering the polypeptide from the medium.

74. (new) A method for producing at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, comprising:

culturing the transformant of claim 72 in a medium to produce and accumulate at least one of an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof in the medium, and

recovering the at least one of the amino acid, the nucleic acid, the vitamin, the saccharide, the organic acid, and analogues thereof from the medium.

75. (new) A polypeptide selected from the group consisting of

a first polypeptide encoded by a polynucleotide comprising the nucleotide sequence selected from SEQ ID NOS:2 to 3431; or

a second polypeptide comprising the amino acid sequence selected from SEQ ID NOS:3502 to 6931;

wherein optionally at least one amino acid is deleted, replaced, inserted or added, in said first or second polypeptides, while having an activity which is substantially the same as that of the polypeptide without said at least one amino acid deletion, replacement, insertion or addition; or

a third polypeptide comprising an amino acid sequence having a homology of at least 60% with the amino acid sequence of the first or second polypeptide, and having an activity which is substantially the same as that of the polypeptide.

76. (new) An antibody which recognizes the polypeptide of claim 75.

77. (new) A polypeptide array, comprising:

at least one polypeptide or partial fragment polypeptide selected from the polypeptides of claim 75 and partial fragment polypeptides of the polypeptides, and a solid support adhered thereto.

78. (new) A polypeptide array, comprising:

at least one antibody which recognizes a polypeptide or partial fragment polypeptide selected from the polypeptides of claim 75 and partial fragment polypeptides of the polypeptides, and a solid support adhered thereto.

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9. (new) A system based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

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- (i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOs:1 to 3501, or at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001, and target sequence or target structure motif information;
 - (ii) a data storage device for at least temporarily storing the input information;
 - (iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOs:1 to 3501 or the at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001, with the target sequence or target structure motif information, recorded by the data storage device for screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information or for screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information; and
 - (iv) an output device that shows a screening or analyzing result obtained by the comparator.

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80. (new) A method based on a computer for identifying a target sequence or a target structure motif derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

- (i) inputting at least one nucleotide sequence information selected from SEQ ID NOs:1 to 3501, or at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001, and the target sequence information or target structure motif information into a user input device;
- (ii) at least temporarily storing said information;
- (iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOs:1 to 3501 with the target sequence or target structure motif information, or the at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001 with the target sequence or target structure motif information; and
- (iv) screening and analyzing nucleotide sequence information which is coincident with or analogous to the target sequence or target structure motif information, or screening and analyzing amino acid sequence information which is coincident with or analogous to the target sequence or target structure motif information.

81. (new) A system based on a computer for determining a function of a polypeptide encoded by a polynucleotide having a target nucleotide sequence, or a

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polypeptide having a target amino acid sequence, derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

(i) a user input device that inputs at least one nucleotide sequence information selected from SEQ ID NOs:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information, or at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;

(ii) a data storage device for at least temporarily storing the input information;

(iii) a comparator that compares the at least one nucleotide sequence information selected from SEQ ID NOs:2 to 3501 with the target nucleotide sequence information for determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOs:2 to 3501, or that compares the at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001 with the target amino acid sequence information for determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from SEQ ID NOs:3502 to 7001; and

- (iv) an output devices that shows a function obtained by the comparator.

82. (new) A method based on a computer for determining a function of a polypeptide encoded by a polynucleotide having a target nucleotide sequence derived from a coryneform bacterium, which is optionally a microorganism of the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and the microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*, comprising the following:

- (i) inputting at least one nucleotide sequence information selected from SEQ ID NOs:2 to 3501, function information of a polypeptide encoded by the nucleotide sequence, and target nucleotide sequence information, or at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001, function information based on the amino acid sequence, and target amino acid sequence information;
- (ii) at least temporarily storing said information;
- (iii) comparing the at least one nucleotide sequence information selected from SEQ ID NOs:2 to 3501 with the target nucleotide sequence information, or comparing the at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001 with the target amino acid sequence information; and
- (iv) determining a function of a polypeptide encoded by a polynucleotide having the target nucleotide sequence which is coincident with or analogous to the polynucleotide having at least one nucleotide sequence selected from SEQ ID NOs:2 to

3501, or determining a function of a polypeptide having the target amino acid sequence which is coincident with or analogous to the polypeptide having at least one amino acid sequence selected from the SEQ ID NOs:3502 to 7001.

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83. (new) A recording medium or storage device which is readable by a computer in which at least one nucleotide sequence information selected from SEQ ID NOs:1 to 3501 or function information based on the nucleotide sequence is recorded, or at least one amino acid sequence information selected from SEQ ID NOs:3502 to 7001 or function information based on the amino acid sequence is recorded,

said computer readable recording medium being optionally selected from the group consisting of a floppy disc, a hard disc, a magnetic tape, a random access memory (RAM), a read only memory (ROM), a magneto-optic disc (MO), CD-ROM, CD-R, CD-RW, DVD-ROM, DVD-RAM and DVD-RW.

84. (new) A polypeptide, optionally derived from *Corynebacterium glutamicum*, having a homoserine dehydrogenase activity, comprising an amino acid sequence in which the Val residue at the 59th position in the amino acid sequence of homoserine dehydrogenase derived from a coryneform bacterium is replaced with an amino acid residue other than a Val residue, or

a polypeptide, optionally derived from *Corynebacterium glutamicum*, comprising an amino acid sequence in which the Val residue at the 59th position in the amino acid sequence as represented by SEQ ID NO:6952 is replaced with an amino acid residue other than a Val residue,

wherein the Val residue at the 59th position is optionally replaced with an Ala residue.

85. (new) A polypeptide, optionally derived from *Corynebacterium glutamicum*, having pyruvate carboxylase activity, comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence of pyruvate carboxylase derived from a coryneform bacterium is replaced with an amino acid residue other than a Pro residue, or

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a polypeptide, optionally derived from *Corynebacterium glutamicum*, comprising an amino acid sequence in which the Pro residue at the 458th position in the amino acid sequence represented by SEQ ID NO:4265 is replaced with an amino acid residue other than a Pro residue,

wherein the Pro residue at the 458th position is optionally replaced with a Ser residue.

86. (new) A DNA, which is optionally a recombinant DNA, encoding a polypeptide of claim 84.

87. (new) A DNA, which is optionally a recombinant DNA, encoding a polypeptide of claim 85.

88. (new) A transformant, optionally derived from a coryneform bacterium, comprising the recombinant DNA of claim 86.

89. (new) A transformant, optionally derived from a coryneform bacterium, comprising the recombinant DNA of claim 87.

90. (new) A transformant, optionally derived from a coryneform bacterium, comprising in its chromosome the DNA of claim 86.

91. (new) A transformant, optionally derived from a coryneform bacterium, comprising in its chromosome the DNA of claim 87.

92. (new) The transformant according to claim 88, which is derived from *Corynebacterium glutamicum*.

93. (new) The transformant according to claim 89, which is derived from *Corynebacterium glutamicum*.

94. (new) The transformant according to claim 90, which is derived from *Corynebacterium glutamicum*.

95. (new) The transformant according to claim 91, which is derived from *Corynebacterium glutamicum*.

96. (new) A method for producing L-lysine, comprising:
culturing the transformant of any one of claims 88 to 95 in a medium to produce and accumulate L-lysine in the medium, and
recovering the L-lysine from the culture.

97. (new) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOs:1 to 3431, comprising the following:

(i) comparing a nucleotide sequence of a genome or gene of a production strain derived a coryneform bacterium which has been subjected to mutation breeding so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogous thereof by a fermentation method, with a corresponding nucleotide sequence in SEQ ID NOs:1 to 3431;

(ii) identifying a mutation point present in the production strain based on a result obtained by (i);

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(iii) introducing the mutation point into a coryneform bacterium which is free of the mutation point, or deleting the mutation point from a coryneform bacterium having the mutation point; and

(iv) examining productivity by the fermentation method of the compound selected in (i) of the coryneform bacterium obtained in (iii);

said gene optionally being a gene encoding an enzyme in a biosynthetic pathway or a signal transmission pathway, and

the mutation point being optionally a mutation point relating to a useful mutation which improves or stabilizes the productivity, or the mutation point optionally being a mutation point which decreases or destabilizes the productivity.

98. (new) The method of claim 97 wherein step (iii) consists of deleting a mutation point from a coryneform bacterium having the mutation point.

99. (new) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOs:2 to 3431, comprising the following:

(i) identifying an isozyme relating to biosynthesis of at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid,

and analogous thereof, based on the nucleotide sequence information represented by SEQ ID NOS:2 to 3431;

(ii) classifying the isozyme identified in (i) into an isozyme having the same activity;

(iii) mutating all genes encoding the isozyme having the same activity simultaneously; and

(iv) examining productivity by a fermentation method of the compound selected in (i) of the coryneform bacterium which have been transformed with the gene obtained in (iii).

100. (new) A method for breeding a coryneform bacterium using the nucleotide sequence information represented by SEQ ID NOS:2 to 3431, comprising the following:

(i) arranging a function information of an open reading frame (ORF) represented by SEQ ID NOS:2 to 3431;

(ii) allowing the arranged ORF to correspond to an enzyme on a known biosynthesis or signal transmission pathway;

(iii) explicating an unknown biosynthesis pathway or signal transmission pathway of a coryneform bacterium in combination with information relating known biosynthesis pathway or signal transmission pathway of a coryneform bacterium;

(iv) comparing the pathway explicated in (iii) with a biosynthesis pathway of a target useful product; and

(v) transgenetically varying a coryneform bacterium based on the nucleotide sequence information to either strengthen a pathway which is judged to be important in the biosynthesis of the target useful product in (iv) or weaken a pathway which is judged not to be important in the biosynthesis of the target useful product in (iv).

101. (new) A coryneform bacterium, bred by the method of claim 97, wherein said coryneform bacterium is optionally a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and

said microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

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102. (new) A coryneform bacterium, bred by the method of claim 98, wherein said coryneform bacterium is optionally a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and

said microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.

103. (new) A coryneform bacterium, bred by the method of claim 99, wherein said coryneform bacterium is optionally a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and

said microorganism belonging to the genus *Corynebacterium* is optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*,

Corynebacterium herculis, *Corynebacterium lilium*, *Corynebacterium melassecola*,
Corynebacterium thermoaminogenes, and *Corynebacterium ammoniagenes*.

104. (new) A coryneform bacterium, bred by the method of claim 100, wherein
said coryneform bacterium is optionally a microorganism belonging to the genus
Corynebacterium, the genus *Brevibacterium*, or the genus *Microbacterium*, and

said microorganism belonging to the genus *Corynebacterium* is optionally
selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium*
acetoacidophilum, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*,
Corynebacterium herculis, *Corynebacterium lilium*, *Corynebacterium melassecola*,
Corynebacterium thermoaminogenes, and *Corynebacterium ammoniagenes*.

105. (new) A method for producing at least one compound selected from an
amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue
thereof, comprising:

culturing a coryneform bacterium of claim 101 in a medium to produce and
accumulate at least one compound selected from an amino acid, a nucleic acid, a
vitamin, a saccharide, an organic acid, and analogues thereof;

recovering the compound from the culture,

said compound optionally being L-lysine.

106. (new) A method for producing at least one compound selected from an
amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue
thereof, comprising:

culturing a coryneform bacterium of claim 102 in a medium to produce and accumulate at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof;

recovering the compound from the culture,

said compound optionally being L-lysine.

107. (new) A method for producing at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue thereof, comprising:

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culturing a coryneform bacterium of claim 103 in a medium to produce and accumulate at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof;

recovering the compound from the culture,

said compound optionally being L-lysine.

108. (new) A method for producing at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid and an analogue thereof, comprising:

culturing a coryneform bacterium of claim 104 in a medium to produce and accumulate at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof;

recovering the compound from the culture,

said compound optionally being L-lysine.

109. (new) A method for identifying a protein relating to useful mutation based on proteome analysis, comprising the following:

(i) preparing a protein derived from a bacterium of a production strain of a coryneform bacterium which has been subjected to mutation breeding by a fermentation process so as to produce at least one compound selected from an amino acid, a nucleic acid, a vitamin, a saccharide, an organic acid, and analogues thereof, and a protein derived from a bacterium of a parent strain of the production strain;

(ii) separating the proteins prepared in (i) by two dimensional electrophoresis;

(iii) detecting the separated proteins, and comparing an expression amount of the protein derived from the production strain with that derived from the parent strain;

(iv) treating the protein showing different expression amounts as a result of the comparison with a peptidase to extract peptide fragments;

(v) analyzing amino acid sequences of the peptide fragments obtained in (iv);
and

(vi) comparing the amino acid sequences obtained in (v) with the amino acid sequence represented by SEQ ID NOs:3502 to 7001 to identifying the protein having the amino acid sequences,

said coryneform bacterium optionally being a microorganism belonging to the genus *Corynebacterium*, the genus *Brevibacterium*, or the genus *Microbacterium*, and

said microorganism belonging to the genus *Corynebacterium* being optionally selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium callunae*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, and *Corynebacterium ammoniagenes*.